

SEARCH REQUEST FORM

Requestor's Name: Ruixiang Li Serial Number: 684725
Date: 9-12-01 Phone: _____ Art Unit: 1646
3D05

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

*Compare Seq ID 1 with
version 1 of ACCOBS 71*

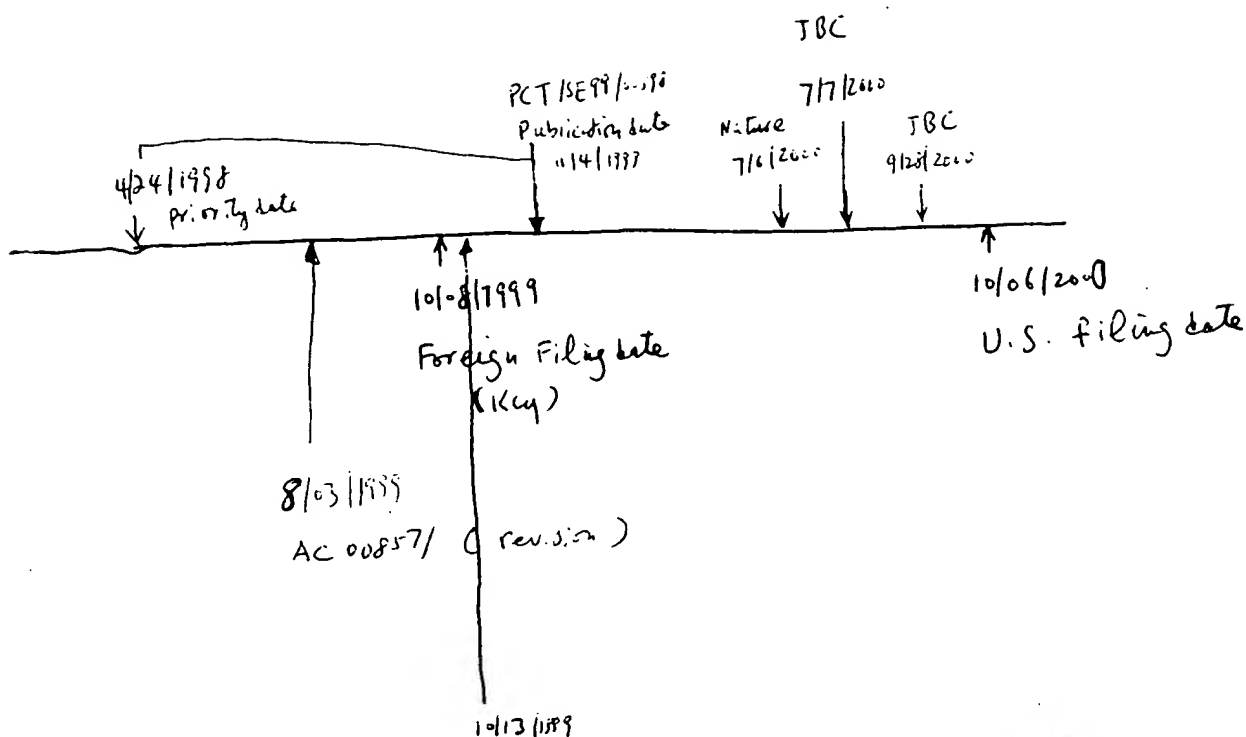
POINT OF CONTACT:
BARB O'BRYEN
TECH. INFORMATION SPECIALIST
STIC CM1 12C14 308-4291

STAFF USE ONLY

Date completed: 9-12-01
Searcher: POB
Terminal time: 130
Elapsed time: prep 40
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site
____ STIC
____ CM-1
____ Pre-S
Type of Search
____ N.A. Sequence
____ A.A. Sequence
____ Structure
____ Bibliographic

Vendors
____ ☒ IG
____ STN
____ Dialog
____ APS
____ Geninfo
____ SDC
____ DARC/Questel
____ GCG Other: Internet



AC 008571
Version AC 008571.1
GI: 5686496

- Submitted (03-Aug-1999)
- ① Public Domain Date:
before 10/13/1999 ?
 - ② Align with SEQ ID 1

Ex Li,

The program I used to compare Seq 1 of 09-684725 to AC 008571, version 1 can only handle 32,000 nt long sequences.

Version 1 is 318,807 nt long, so I had to break it into 7 parts & compare each of the parts to Seq 1.

Bases 204888-205616 match the complement of Seq 1.

Barb



CGCTCAGGATAGGACTTCGGTCCCTAGGATCGGATCCCCGGGCTATATATAGCTCCATCGATC
 TTCTCTATATCGGCGGATATGGGATATATACAGACACATCTCCGCGATAGCATGCTGATCTA
 TCCCATCT
 CACAGACATACCGCTCTCACTTCTTACTAACCAATTCGCGAGGGCGGCGATCTCTCTCTCT

PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search <input type="text" value="Nucleotide"/> for <input type="text"/>							<input type="button" value="Go"/> <input type="button" value="Clear"/>
Limits		Preview/Index		History		Clipboard	
Details							
Display <input type="text" value="GenBank"/>		as <input type="text" value="HTML"/>		<input type="button" value="Save"/>		<input type="button" value="Add to Clipboard"/>	

☐ 1: AC008571[gi:5686496]

LOCUS AC008571 218807 bp DNA HTG 26-JAN-2000
 DEFINITION Homo sapiens chromosome 5 clone CTC-550M4, LOW-PASS SEQUENCE
 SAMPLING.
 ACCESSION AC008571
 VERSION AC008571.1 GI:5686496
 KEYWORDS HTG; HTGS_PHASE0.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 218807)
 AUTHORS DOE Joint Genome Institute.
 TITLE Sequencing of Human Chromosome 5
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 218807)
 AUTHORS DOE Joint Genome Institute.
 TITLE Direct Submission
 JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 COMMENT [WARNING] On Mar 9, 2000 this sequence was replaced by a newer
 version gi:7211884.
 -----Genome Center
 Center: Joint Genome Institute
 Center Code: JGI
 Web site: <http://www.jgi.doe.gov>

* NOTE: This record contains 42 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.

* 1 760: contig of 760 bp in length
 * gap of unknown length
 * 761 1587: contig of 827 bp in length
 * gap of unknown length
 * 1588 2375: contig of 788 bp in length
 * gap of unknown length
 * 2376 3130: contig of 755 bp in length
 * gap of unknown length
 * 3131 3929: contig of 799 bp in length
 * gap of unknown length
 * 3930 4664: contig of 735 bp in length
 * gap of unknown length
 * 4665 5908: contig of 1244 bp in length
 * gap of unknown length

Ex. Li -

This sequence
 record was 59 pages
 long, so I didn't print
 all of them, but wanted
 to show you that I was
 able to retrieve the
 correct record.

Barb

```
*      5909      6642: contig of 734 bp in length
*                  gap of unknown length
*      6643      7928: contig of 1286 bp in length
*                  gap of unknown length
*      7929      9764: contig of 1836 bp in length
*                  gap of unknown length
*      9765     11784: contig of 2020 bp in length
*                  gap of unknown length
*     11785     13491: contig of 1707 bp in length
*                  gap of unknown length
*     13492     15107: contig of 1616 bp in length
*                  gap of unknown length
*     15108     17115: contig of 2008 bp in length
*                  gap of unknown length
*     17116     18946: contig of 1831 bp in length
*                  gap of unknown length
*     18947     20113: contig of 1167 bp in length
*                  gap of unknown length
*     20114     21818: contig of 1705 bp in length
*                  gap of unknown length
*     21819     23699: contig of 1881 bp in length
*                  gap of unknown length
*     23700     26482: contig of 2783 bp in length
*                  gap of unknown length
*     26483     29112: contig of 2630 bp in length
*                  gap of unknown length
*     29113     32185: contig of 3073 bp in length
*                  gap of unknown length
*     32186     35668: contig of 3483 bp in length
*                  gap of unknown length
*     35669     38521: contig of 2853 bp in length
*                  gap of unknown length
*     38522     41445: contig of 2924 bp in length
*                  gap of unknown length
*     41446     44435: contig of 2990 bp in length
*                  gap of unknown length
*     44436     49095: contig of 4660 bp in length
*                  gap of unknown length
*     49096     52340: contig of 3245 bp in length
*                  gap of unknown length
*     52341     58964: contig of 6624 bp in length
*                  gap of unknown length
*     58965     67289: contig of 8325 bp in length
*                  gap of unknown length
*     67290     76424: contig of 9135 bp in length
*                  gap of unknown length
*     76425     82934: contig of 6510 bp in length
*                  gap of unknown length
*     82935     92710: contig of 9776 bp in length
*                  gap of unknown length
*     92711     99976: contig of 7266 bp in length
*                  gap of unknown length
*     99977    111110: contig of 11134 bp in length
*                  gap of unknown length
*    111111    119820: contig of 8710 bp in length
*                  gap of unknown length
*    119821    131057: contig of 11237 bp in length
*                  gap of unknown length
*    131058    140629: contig of 9572 bp in length
*                  gap of unknown length
*    140630    155583: contig of 14954 bp in length
*                  gap of unknown length
*    155584    167555: contig of 11972 bp in length
*                  gap of unknown length
*    167556    184185: contig of 16630 bp in length
```

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*          gap of unknown length
* 184186   201363: contig of 17178 bp in length
*          gap of unknown length
* 201364   218807: contig of 17444 bp in length.
FEATURES             Location/Qualifiers
     source            1..218807
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /chromosome="5"
                        /clone="CTC-550M4"
BASE COUNT    66620 a 42793 c 41952 g 67204 t    238 others
ORIGIN
1 gatataatat cgatcccctc actggctcta aagaacaaat acagcaacgt ggatttcaat
61 taagattctg ccatcccatc gatagagttc tcttaatcct tctttagagg tgctgcctgg
121 gtaataaaac cttcatgctg caggctgtag gcaggtttgt ttaacccgag cttaaactgac
181 aaagctctct gagacatgct cacctgctta gaatctgtgc atcacctcct attggctgtg
241 tgtggggcat tgcgatgcct ccatgtggta caggaggctg gcctaagagt tctgaactgc
301 aaaccttcac aggaaattct tgggctggct ggccacctgg cttacgttat ttattttatt
361 atttagttag ttgtttttat tgcttttagg gtctgcacct gatggtggca gtgagggagg
421 ttgaggtgag cttccatctc ttggaatccc accattccta ttcaactcat gtcaaattaa
481 attaatacta tttccatgtg aataattgaa gatatttcct caactttaaa aatgtgaaaag
541 aaggcatctt ttagaaaata tttgctgttt aaaaaatact agccatgcac aatccagata
601 agaagaatgt agtttgagac gagttcctgt gaagattatc accctaagcc actcctgtat
661 atatgtttcc ctactgacac ctgctcatcc ttctttgctt cattctatgg
721 ttaactccta agcacaggga tgcaattctg tctggagatc gaagagaaaa ggagggnggg
781 ggnnnnnttt agaaccctn gatgtgacgc atcgctaagt gctctaaatg taccagcct
841 tacaacata ttctatcact ccatgtctg tgaccatagc agaaattagc aatcaatcat
901 agaagtgtgt cctcctgggc ctggatgtgg cttcacaaat tctcacagcc actgtaccag
961 tgggtcagac tctaaaccga ggaatacaca tgtacacacg cagatacatg ggtgtgtgtg
1021 tttgtgtgtg tgtgtgtttg ttttaatat ataaggccct atattcctga tggtgacttt
1081 gaaaaaaatc acttgtgctc tgtggtccta agtttttttt tttttttatc tgaaaagagga
1141 aatttgagtt ctttagtcta ctagtgtgaa aagcacaaag ggcctgtcac tgcagtgtgtg
1201 ttttctgggg ctcaagttaa caagagacaa atcacagatt caatcaaaag ctgcatgtgg
1261 aaggctcaat accatttttt gagaaaagga aaccttgggg ttattcatct tcacctcata
1321 ggaatcaagc agaaatagaa attaccttcc aggagaagga atatataact tacagctttt
1381 tgagatcggc ttacatttta ttttttctta ttcaatctag ttcctttatg gaacataaat
1441 taaccttaaa gagtagcact ggagaagagg gaaagaatat tgcgatttct ctctctctac
1501 aatttaaagt ttaaaaatca tagttatctt ttctttattt atcaaaaggc tatgacctct
1561 cagagcaatt gtgtaagcaa cccaaaaggg ggnatagggg nttcgtagac gtactcctat
1621 agtgctctaa agcttgggat gaggttattt gcatatgtgt tcttagatac gttgaacaac
1681 aagaatgccca agataatcct gaatcctttg ggattacaca agtggcccat tttcccttac
1741 ttgatggctg tgaagaaacc ctaagtgcag taggtccctt aaaatgcaat gctggctttt
1801 ctgaggatct atcctaacct cttttctagg caccagatca ataactcatg taacatctca
1861 tcatgaccca actggaaaag ttacggatat gctaaaagag aagatggagt ctgagccagt
1921 ggaaccataa atgtgggtta cacgttctgg aacctagaga atctttgtgt tagataaagg
1981 tggagaggaa tggattataa agttaggtaa gaggatttgt tggatatggga cagtattctc
2041 aggcaagatt taacacactg aaaagactct gggagaaggt tctaataatt tgccacaagg
2101 tgggggaaaa atttaaaaaa tttttttttt tttttttgaa actggaaaag acataccaac
2161 cttaaaaaatg aaatagcaaa attgccttgc caactgggga gaatagatca acaggcacgg
2221 agaaatgggt atactagaat gtttctactt catatttaaa aaactactgg ctgattaaat
2281 tcctcaaaag ggctcagagg acgttcattt tactaaagaa ttaaaaaatg cagtacctac
2341 aacactgctc caaagaaagc aacgggccag gttttccagc gacttgttgc cgatccctaa
2401 nactctaaat agcagnnngn ncaaccacaac cttaactgac aaagctctct gaaacatgct
2461 cacctgctta gaatctgtgc atcacctcct atnggctgng tgtggggcat tgcgatgcct
2521 ccatgtggta caggaggctg gcctaagagt tctgaactgc aaaccttcac aggaaattct
2581 tgggctggct ggccacctgg cttaggttat ttattttatt atttagttag ttgtttttat
2641 ttggttttag gtctgcacct gatggtggca gtgagggagg ttgaggtgag ttcccatctc
2701 ttggaatccc accattccta ttcaactcat gtcaaattaa attaatacta tttccatgtg
2761 aataattgaa gatatttcct caactttaaa aatgtgaaaag aaggcatctt ttagaaaata
2821 tttgttgttt aaaaaatact agccatgcac aatccagatt agaagaatgt agtttggag
2881 gagaaaaccc ccccgaaaaa aataaaaaaga aaatttcctg gaagatatca cctaagcact
2941 ctttatatag tttccctact gacacctgct catccttctt tgctcattga cagcatctag
3001 tggtagctct agccagngat ccattctgcc tgagatcaga tatcctccaa gagcacaac
3061 aggtagaaat ggcattcata taggggctgt acagtgtgtt gctgagagat gtatataaat
3121 ttcttgagat acgaaagtc tccgccgtca tctaacatct caaanacan aannatggct

```

GAP of: us-09-684-725-1/ check: 1088 from: 1 to: 729
 FROMIC of: /home/bobyren/big/US09684725.seq
 sequence 1, application us/09684725

general information:
 applicant: lee harland
 title of invention: novel polypeptide
 file reference: pcs10361adam

to: version1 check: 7472 from: 1 to: 32000

Symbol comparison table: /opt/gcg/gcgcore/data/rundata/nwsgapdna.cmp
 Compcheck: 8760

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000
Quality:	2550	Length:	32019
Ratio:	3.498	Gaps:	8
Percent Similarity:	43.239	Percent Identity:	41.268

Match display thresholds for the alignment(s):

IDENTITY
 5
 1

us-09-684-725-1 x version1 September 12, 2001 10:31

```

1 .....atggaaaacttcagaatgtctct 25
6751 ttctacctttaagtcagggtacatgacagatgacagatctgtta 6800
26 ggaatccacagacaagaatgaagatccatccagaacacctgacagc 75
6801 catagctaaacatgtgcattgtgattagctaacacagattaccatcac 6850
76 accgagagatctgcgccttcctctgcgacccgcgcgacacacttct 125
6851 caaagtgttaagccacagatccattagctattcttcctgatactctcc 6900
126 cctcccgctgctgtgtgt...atgtgcacattttgtgtggtgggtca 172
6901 cctcccaacccttaccctctgacaggtccagtggtgttccctcc 6950
173 ttggcaatgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 222
6951 ctgg.....gttcagtgttccatcaltccagctccacattataagt 6992
223 accgccacaactactactcttcagccctgcggtctctgacctctgt 272
6993 gataacatgcagtatattgtattctgtc...cctgcattagtgtgtgaa 7039
273 cctgctccttggaatgcccctggaagtcatagtatgtgcgcaactacc 322
7040 gataatggtctgcagctccatccatcaltgltcccgtaag...gacacgata 7085
323 cttctctgttcgggcccgtggctgctacttcaagaagcgccctcttgag 372
7086 ttgttctcttcgagatgagatttgcctcgttgcgcaggtcgtgagtgca 7135
373 accgtgtgtctgcctccatccatccacacacacacacacacacacac 422
7136 atggtgcagatctgtgcacacacacacacacacacacacacacacac 472
423 ctacgtggcctcctacacccgttcgcgcgccaactgcagaagacccggc 472
7186 tctctgtcctcagcctcccaagtagcttggattacag...gcatacgcc 7231

```

```

473 gccggccctcaggaatcctcgcatcgtctg.....gggtcttcgcg 514
7232 accagaaccggcctaatttttttttttttttttttttttttttttttt 7281
515 tgcctctcctccctgcc...aacacagatccatgcatcacaagttccac 561
7282 tgttgcgcaagctgtgtctgaactcctgaactcaagtatcaccactgct 7331
562 tacttcccgaatggtccctgttcccaagttccgacacgtgaag.... 607
7332 cagctcaccaaagtgcgtggattacagaagtgaagccacctgcctgtgta 7381
608 ..tcatcaagccaatggtgatctacaattcatcatcaggtaacctcc 654
7382 tctcattctcttttatgtcgtcatagatttccatggtgtatataccatat 7431
655 ttccattctacccctcccatgactgttcatcagtgctccttactacct 704
7432 ttcttattcagtcatttttatgtatgacagtgatgtagcagagmnnnn 7481
705 catgcaactcagatgagtatctag..... 729
7482 ctnnnnnngannanacatttttaaggtatatatttgggtgctaatactgt 7531

```

GAP of: us-09-684-725-1, check: 1088 from: 1 to: 729

FROMIG of: /home/bobryen/big/US09684725.seq
sequence 1, application us/09684725

general information:

applicant: lee harland

title of invention: novel polypeptide

file reference: pcs10361adam

to: version1: check: 7472 from: 32001 to: 64000

Symbol comparison table: /opt/gcg/gcgcore/data/rundata/nwsgapna.cmp
Compcheck: 8760

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: 0.000

Quality: 2598

Length: 32001

Ratio: 3.564

Gaps: 4

Percent Similarity: 39.423 Percent Identity: 35.852

Match display thresholds for the alignment(s):

1 = IDENTITY
5
1

us-09-684-725-1 x version1 September 12, 2001 10:25

```
1 .....atgaaaa 8
48451 atgggtggatcttcaaggatgctcaggtccctggaacagtgaa 48500
9 acttcagaatctctcctggaatccagcagagaactagaaatcatctcc 58
48501 cctccagatagaatcagagctcagcgaatgataaattgtaalg 48550
59 agaaacacctgaacagacccagagagatctgagctctcctcgagact 108
48551 gggacacacccaatgctcagctgtagcttgatctctgaggagacttcc 48600
109 cggcgagccctctctccctcccgctgctggtgtatgtgccaatttc 158
48601 ccaatgaaaaaagaagcaggttgagatctctgtgaggttacatt 48650
159 tgtgtggggatcatgtgcaatgtccctgtgtgctgtgttctg.... 204
48651 ccataagaagaagagctgcctcgcagatgtagacttgatttctgatat 48700
205 .....cagcaccaggctatgaagacgccaccactactactcttc 246
48701 gacagcttcctccactagatgctagtgaaagtgtagcaggaagc 48750
247 agcctgctgctctgactctctgtctgtctcttgaaatgcccctgga 296
48751 agaatagtgtagcagcagcagctagcaattaggaaglaagccaccgc 48800
297 ggtctatagatgtgctgcaactacccttctgttcgggcccgtgggt 346
48801 gtgactcgtgtaggaggaagcagctctgaaagtgacactcttgact 48850
347 gctactcaagaagccctcttgagacgctgtcttcgctccatcctc 396
48851 acttc.tcaccagctgtctctagagtaactcaactgtccagctctca 48899
397 agcatcacaccgctcagctgtgagcgtctacgttgccatccataccggt 446
48900 acatctgactgccactgcatgttcaagltgtgtaacataatattgtgc 48949
```

```
447 ccgggc.caactgcagagcacccggcgccgcccctcagatcctcggc 495
48950 ttacactgagagaatataaccactagatgaactctcagagagaataactc 48999
496 atgcttgaggctctcctccgtctctctcctcctgccaacaccag..... 539
49000 ttctgttaacatttaaggtctcctctcatcatcagatagaactgtgatta 49049
540 ....catccatgcatcaagttccactactcctcccaatgggtccctgctc 585
49050 agttaccaccagcttaacatcagttccccaagtacaacacccctctgggn 49099
586 ccaggttcggccacctgtacggtcatcaagcccatgtgactcaaatlt 635
49100 nggggggngngnggggggggngngngngngnggttggttgggt 49149
636 catatccaggtcaactctctcctactatctactcctccctcctgactgca 685
49150 cgattngaatgttntctngttagngngngngngngngngngngatcatt 49199
686 tcaatgtctctactactactcactgagcactcagagtgagatctag..... 729
49200 gctctgacctgaatgtgttctctcctcagcatatctgctcctcttgta 49249
```

GAP of: us-09-684-725-1 check: 1088 from: 1 to: 729
FROMIG of: /home/bobryen/Big/US09684725.seq
sequence 1, application us/09684725

general information:
applicant: lee harland
title of invention: novel polypeptide
file reference: pcs10361adam

to: version1 check: 7472 from: 64001 to: 96000

Symbol comparison table: /opt/gcg/gcgcore/data/rundata/nwsgapdna.comp
Compcheck: 8760

Gap weight:	50	Average Match:	10.000
Length weight:	3	Average Mismatch:	0.000
Quality:	2460	Length:	32000
Ratio:	3.374	Gaps:	4
Percent Similarity:	36.900	Percent Identity:	36.900

Match display thresholds for the alignment(s):

1 = IDENTITY
- = 1

us-09-684-725-1 x version1 September 12, 2001 10:34

```
1 .....atgaaaaac 10
89801 ataatctctcttctctgtgttgactgttaacctatgttgggtgtctg 89850
11 ttccagaatgtcttctctgtatctacacagacagaaactagaatccattccag 60
89851 ctggaagaacatgagacacctgttccaatatgatatagaggtccagggc 89900
61 aaacacctgaaacagacacgagagatcttgacctctctcttcgagacctg 110
89901 tggaaagaatttgagagtgtagcctttaaagtcttgcgtgtagcgca 89950
111 gcgcagccactcttctcccgctgctgtgtgtatgtgccaatcttg 160
89951 tccctttttaacaacagaaatttttctcaatttgcctctgtgtca 90000
161 tggctgggggcatctggcaatgtctgtggtgcggatgtatgcagcac 210
90001 cgctccctgaaacgtgaatcaactacatctttaggtatctcttgaca 90050
211 caggctatgaaagcgcacccaactactactcttcagcctgcggtctc 260
90051 gtgtcagctctgctttaaagctccctttttaaacttaagcttgact 90100
261 tgaactctgtctctgtctcttgaaatgccctggaaggtcataagatgt 310
90101 ttctcttctgtctctctgtgtatgtgcaaaaaaacaagcgttggttt 90150
311 ggcgcaactaccct...tctgttcggggccggtgggctgtactaacg 357
90151 ttctatactatagtttatatatattttggagcagagatgacaatacaca 90200
358 acggccctcttggagacggtgtgcttgcctccacacctcagcatcacac 407
90201 tactctgcttctgtctgtgctgcatcttacttaaatctgacttatt 90250
408 cgtcagcgttgagcgtacgtggtccatctacaccggttcggcgccaaac 457
90251 tatcagattttaactcagcaacttctctcagaacacctgccaatgacc 90300
```

```
458 tgcagagacccc-ggcggcgccctcagatctctcggcatcgtctggg 506
90301 cagacaacacccctgttttatgcatccacagcacccctgaattctctttg 90350
507 ctctcgtgtctcttctccctggcccaacacacagacatccatggtcacaagt 556
90351 cagcccttgttcaaccagcaattatcacagagataattatgtttctcaca 90400
557 tccaacttccccaatgggtc....cttgtccaggttcggccacct 601
90401 agtatataattctatgaggggcaggacctgtgtctgattcacacaaagt 90450
602 gtac-ggtcatcaagcccaigtgatctacaaatttcacatccacaggtcac 650
90451 atactagctactgtgcttaatgacatttatcaaaactctatggagcat 90500
651 ctcttctatcttaccctccccaactgacgtatcagtgctctctact 700
90501 ctctcgtgtacagccatgtagtactgtgaaacagatagattagctctc 90550
701 acctcatggcaactcagagtgagtagtctag..... 729
90551 agctcgtgaaactatagctcagtgaggttttcaattcttcttttccccc 90600
```


GAP of: us-09-684-725-1 check: 1088 from: 1 to: 729
 FROMIG of: /home/bobryen/Big/US09684725.seq
 sequence 1, application us/09684725

general information:
 applicant: lee harland
 title of invention: novel polypeptide
 file reference: pcs10361adam

to: version1 check: 7472 from: 96001 to: 128000

Symbol comparison table: /opt/gcg/gcgcore/data/rundata/wsgapdna.comp
 CompCheck: 8760

Gap Weight: 50 Average Match: 10.000
 Length Weight: 3 Average Mismatch: 0.000
 Quality: 2441 Length: 32001
 Ratio: 3.348 Gaps: 6
 Percent Similarity: 38.187 Percent Identity: 38.187

Match display thresholds for the alignment(s):

IDENTITY
 5
 1

us-09-684-725-1 x version1 September 12, 2001 10:28

```

1 ..... atggaaaacttcagaatgtctctgat 29
105351 tgcacgtgagctctctgctgtagtattcttcttcttctctctgc 105400
30 ctaccagcagaactaagaatccatccagaacacttgacagaccg 79
105401 tgaacaaaca.caagtcaactgtctccagattctataactctatacaact 105449
80 aggaagtatcggc..cttctctcggaacctcgcgacagcactcttcc 127
105450 actactcttctccgaacctcaacagcaaatctgtagcacttcagct 105499
128 tccccggtcgtgtgtatgtgccaattttgtgtgtgggtgctatggc 177
05500 tgcgtctatctctccacagatattcttactctgtctgtagtaatttt 105549
178 aatgtcctgtgtgtgtgtatctgacagaccaggtatgaagagcc 227
105550 tcaagcacgltcaacattctgttctatccagtagtcaataatccatc 105599
228 cacaactactaactctctcagcctggtctgtacctctgtctgtc 277
105600 cagtcactctcgaagctgacatcaactaaactaccagactgtgca 105649
278 tccctggaatgcccttgaggtctatgtagatgtgagcgcaactacccttc 327
105650 gaagggagagagcttccatgtctcctgtagtctctatcttggaatccatc 105699
328 ttgttcggcccggtggcgttacttcaagaagcgccctcttgagaccgt 377
105700 tctatgaagaagctgtgaaatgttatttggatagtcctcctcctgaatag 105749
378 gtgcttgcctccatctcagatcaacacacgctgagcggtacg 427
105750 ccagtgctataaagaacaattcagaagtagtactgtctaataatgaatt 105799
428 tggccatcttaaccggttccgagcaactgacagacaccggcgccgg 477
105800 taticcaaccctgaactttctatttcatgtgacatcttctctaatgac 105849

```

```

478 gccctcaagatcctcgcatcgtctggggtctctcgtctctccct 527
105850 aatctctactcatctgtgtcaccctgtgtatatacacaactgaacct 105899
528 gcc..caaccacagcatccatggacatcaagttccactact....cccc 570
105900 tcccttagtataactacttactctcaaaatcaactatttatatactc 105949
571 aatgggtccctggtccaggttcggcaact..gtacggatcaagacc 618
105950 attgagatcataatcttctatcttctagtgtgtcttctcaattatctc 105999
619 atgtgacttacaatttcaatccaggtcaacctctctctatctact 668
106000 attgtaactactctgtttgttaactcttctatcttcccttctctatct 106049
669 cctcccaatgactgtcactcagtgctcttactacc..taatgacactaga 717
106050 ccttcttaatctccacagatattttaaacaccccttaatgacactcca 106099
718 gtgagtactag..... 729
106100 ttgttctctattctattcttcttgaatttttttcaatgaccttcaagc 106149

```

GAP of: us-09-684-725-1 check: 1088 from: 1 to: 729

FROMIG of: /home/bobryen/Big/US09684725.seq
sequence 1, application us/09684725

general information:

applicant: lee harland
title of invention: novel polypeptide
file reference: pcs10361adam

to: version1 check: 7472 from: 128001 to: 160000

Symbol comparison table: /opt/gcg/gcgcore/data/rundata/nwsgapdna.comp
CompCheck: 8760

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: 0.000

Quality: 2461 Length: 32002
Ratio: 3.376 Gaps: 9
Percent Similarity: 42.641 Percent Identity: 42.641

Match display thresholds for the alignment(s):

1 - IDENTITY
5
1

us-09-684-725-1 x version1 September 12, 2001 10:36

```
1 .....atgaaactcagaatgtctctgatatc 32
156901 aagagggaataactataatgaataatgaatgaatcctaaagatg 156950
33 ccagcagaactagaagatccatccagaacaacatg..... 69
156951 tggagacgtgattgattgagctggaagaagatgctcctgaggttct 157000
70 .....aacagccgagagatctgacctctctgcgagac 107
157001 gaccagtgctaaatgacgtggcgcttcaactttaagaagaacat 157050
108 tcgsgcagcgaactctctctcccgctcgtgtgtatgtgcaattt 157
57051 tagaggtggaaggttccagagaagaagaatctccttgcataat 157100
158 ttgtgtgggggtcattgtgcaatg..tcctgtgtgctgtgattctgc 205
157101 aagaggttccatcgttgggggtgactgacgtgactatgcatcaga 157150
206 agcaccaaggtatgaagagcccaactaactaactccttcagccctg 255
157151 ttcccca.tcaggaatgagctcctccactattgctttagagcagg 157199
256 gtctctgacctcctgtctcctcttgaaatgcccctggaagtctatga 305
157200 gtccccaaccccccagccacagacagatccatcagcctgttaga 157249
306 gatgtggcgcaactaccccttctctgttcggcccggtggcgtgctatca 355
157250 actgtgtcacaagggaaggtgagtgacgggcaagcagtgcttacctga 157299
356 .....agacggccctcttgagaccgtgtgtctcgcc.tc 389
157300 gctcatgcaaggatcagtgctctctttagaatacctaactaagcctta 157349
390 catctcagcatcaaccgtcagcgttgagcgtcagtgagcctcctaac 439
157350 tgatctgaggtggaacagtttatctctgaacaacatcctcccaattctc 157399
```

```
440 accggttcgcgcacaacttgagagcaccgcgcgcgggcccctcagatc 489
157400 cctctctcccgcaagaacagtggaataaactgtcttccacaataaccatc 157449
490 ctgg.....catcgtctggggtctcctcgtgtctcttctcccgccaa 533
157450 ctgggtgcgaataaacgttgggggtgctggaagaatgtctcagctgaa 157499
534 .....caccagatcattgcatcaagttccactaacttcccca 572
157500 gaagtgtgtctcactgtccatccatcagtgactcgagagataaagatcccca 157549
573 tgggtccctgtgtcccaaggttcggccacctgacgtgcatcgaagccatgt 622
157550 ttcaagccaactcagagcagctctgaggggtcagttcagc.tgacaggt 157598
623 ggaatcaattcattcatcactcaggtcactcctctcat.tctactcct 671
157599 cctggggcgtctgcatctcccttggccccactacttctgttcttct 157648
672 cccatgactgtcatcagtgctcctctactactcaatggcactcagatga 721
157649 ttccagatgtgatacctcagagacttcatgtcctaataaagcctgactgc 157698
722 gtaactag..... 729
157699 taattcccccaagagctgtgtgcttgagcaacaacaacgtgtgacacag 157748
```

GAP of: us-09-684-725-1 check: 1088 from: 1 to: 729
FROMIG of: /home/bobryen/big/US09684725.seq
sequence 1, application us/09684725

general information:
applicant: lee harland
title of invention: novel polypeptide
file reference: pcs10361adam

to: version1 check: 7472 from: 160001 to: 192000

Symbol comparison table: /opt/gcg/gcgcore/data/rundata/nwsgapdna.cmp
CompCheck: 8760

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: 0.000

Quality: 2515 Length: 32005
Ratio: 3.450 Gaps: 5

Percent Similarity: 38.812 Percent Identity: 38.812

Match display thresholds for the alignment(s):
- IDENTITY
- 5
- 1

us-09-684-725-1 x version1 September 12, 2001 10:30

```
1 .....atggaaaactcagaat 18
178551 tttagaggaagatcacagatgtaagtgccattttatcacatcacat 178600
19 gcttcctggatccacagcagaactagaa.....gatccattccagaa 63
178601 tgggtacgacatatacaacatgattatgactatcgatgtgcccttgat 178650
64 cacttgaacacgacagagatatactggccttcctctcggacctcgcg 113
178651 cacttggcagaggtagaggtttccaggtttccactataaaacccctca 178700
114 cagccactctctcctcccggtctgtgtgtatgtatgtcccaattttgtg 163
178701 cccctatagttctacactgtatctcgggaagaagatcatgattgaa 178750
164 tgggggtcatggcaatgtcctgtgtgtcctggtgatcttcgacacag 213
178751 .cctaacgtgagaagtgggaagtgtgtctgtcttcttgagggcagag 178799
214 gctatgaagcgcacccaactactactcttcagcctggtcgtctctga 263
178800 tatctaacataattatttgaattttctgtatggagggtttgtcccttc 178849
264 cctcctgtctgtcctctggaatgcccc...tggagttctatgagaatg 309
178850 tccccactatattatattatcaatcatcttttatatcacatagact 178899
310 tggcgaactaccctctcttctggtggccgtgggtctactcaagac 359
178900 gtgatatattttgttactttgggtatatactcaatactacttatttt 178949
360 ggccctcttgagaccgtgtgtctgcctcactcctcagacatcacacag 409
178950 gtgtcgaagtagttcagcttgattatgtatgtgcgtgtgtgccttt 178999
410 tcagcgttgagcgtcagctggccatccataaccggttcgcggccaaactg 459
179000 ggcatactcaatcacctgtgaccttcttctcctcctccttcttctt 179049
```

```
460 cagagcacccggtcgccgtccctcagatcct.cggcatcgtctggygct 508
179050 cccctccctatttctcgttactacaagatgtccatgctcatcttaata 179099
509 tctcgtgtcttctcctcctcgtcccaacacacagatccatcagatcaagtc 558
179100 tctctactcaatccctagaaatcattgttcttctcgtggtcggtgttc 179149
559 cactacttccccaatgggtccctgttcccaagttcgcgcacactgtaaggt 608
179150 ttttattagagaatgtgtgtggaactaagatcgtatatttttttaat 179199
609 catcaagccatgtggatcctacatlttaicatatccaggtcaccccttcc 658
179200 tggagaaggcatcggaaacaaagatctgagtacaaggtaatttcttga 179249
659 tatictaacttcccccagatgacatgacatgcttctctactactcatg 708
179250 tacttga...gtctccctgtctcagcccttattatctgacagacag 179295
709 gcaactcaagtgagtactctag..... 729
179296 gaatgtatgtgagtatatataatataatgatatatgatagagggttgg 179345
```

GAP of: us-09-684-725-1/ check: 1088 from: 1 to: 729

FROM: /home/bobyen/big/US09684725.seq
Sequence 1, application us/09684725

General information:

Applicant: Lee Harland

Title of invention: novel polypeptide

File reference: pcs10361adam . . .

to: version1, check: 7472 from: 192001 to: 218807

Symbol comparison table: /opt/gcg/gcgcore/data/rundata/nwsgapdna.cmp
Compcheck: 8760

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: 0.000

Quality: 2610 Length: 26807
Ratio: 3.580 Gaps: 0

Percent Similarity: 35.802 Percent Identity: 35.802

Match display thresholds for the alignment(s):

1 - IDENTITY
: - 5
: - 1

us-09-684-725-1 x version1 September 12, 2001 10:39

```
1 .....atgaaaaacttcagaaatgcttcctgata 32
204901 ctgagtcgcatgagtagtagagagacactgtagacatgcatgaggagag 204950
33 ccagcagaaactagaaagatccatccaaacaaactgnaacagcacagag 82
204951 gtaagaataggaagagtgaccctgagatgaatgttagatccaatg 205000
83 agtatctgctctctctgacacacacacacacacacacacacacacacac 132
205001 gcttgatgacccgtaacagtgacacacacacacacacacacacacacac 205050
133 gtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 182
205051 aagtagtgaaacttgatgcatgcatgctgctgctgctgctgctgctg 205100
183 cctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 232
205101 cagcagaaagcccaagacgacgacgacgacgacgacgacgacgacgacg 205150
233 actactactctcagcctgctgctgctgctgctgctgctgctgctgctg 282
205151 tgcctgagcttgctgctgctgctgctgctgctgctgctgctgctgctg 205200
283 ggaatgccccggaaggtctatgagatgtgctgctgctgctgctgctgct 332
205201 acgctgacggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 205250
333 cgggcgcgtggtgctgctgctgctgctgctgctgctgctgctgctgctg 382
205251 gagggcgcgtgctgctgctgctgctgctgctgctgctgctgctgctg 205300
383 tcgctcctcatctcagcatccacacacacacacacacacacacacacacac 432
205301 tgcgcacacatctcatagacctcctcagggggtcctcagagacagacag 205350
433 atcctaacacgcgttccgcgcacacacacacacacacacacacacacac 482
205351 agtcaagagacgcgcaggtctgaagagtagtagtgtgtggtgcttcat 205400
```

```
483 cagatcctcggaatcgctggtgtcttcctgctgcttctcctcgccca 532
205401 agcctgtgtctgcagaaatcaccagcgcacacacagacatctgcacatgacc 205450
533 acaccagcatcctgcatcaagttccacactcctcccaatggtccctg 582
205451 ccaccacaaaattggcacaatacaccacagacacagggaggaagaagtgg 205500
583 gtcccaagttcgcgcacacctgtacgtatcaagcccatgtgatctaca 632
205501 ctgcgcagaggtccgcagaggaagccagatcctcctgctgctgctcag 205550
633 ttcatcatcaggtcaactcctcctcctcctcctcctcctcctcctcctc 682
205551 gtgttctggaatggaatcttctgctgctgctgctgctgctgctgctg 205600
683 tcatcaggtcctcctcctcctcctcctcctcctcctcctcctcctcctc 729
205601 tctgaagtttccatcctcctcctcctcctcctcctcctcctcctcctc 205650
```


GAP of reverse of: us-09-684-725-1 check: 1088 from: 1 to: 729
 FROMIG of: /home/bobryen/big/US09684725.seq
 sequence 1, application us/09684725

general information:
 applicant: lee harland
 title of invention: novel polypeptide
 file reference: pcs10361adam

to: version1 check: 7472 from: 32001 to: 64000

Symbol comparison table: /opt/gcg/gcgcore/data/rundata/nwsgapdna.comp
 CompCheck: 8760

Gap Weight: 50 Average Match: 10.000
 Length Weight: 3 Average Mismatch: 0.000

Quality: 2575 Length: 32000
 Ratio: 3.532 Gaps: 3
 Percent Similarity: 38.409 Percent Identity: 34.842

Match display thresholds for the alignment(s):

IDENTITY
 5
 1

us-09-684-725-1 x version1 September 12, 2001 10:44

```

729 .....ctagatactcaactctgaagtcagtgccatgaggtgtagtagaacctgat 685
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48451 atgggtgggaatttcagaggaattgtcaggttccctggaacaacgtgaa 48500
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
684 gacagtcagtggaaggaagtagaataaggaaggaagtgacccgtagatga 635
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48501 cctcagaataaatacagaagctgcagcgcaatgtatataatgtttaatcg 48550
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
634 aattgatacaccacatggcttgatgacgtacaggtgcccgaacctggg 585
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48551 gggacaaccacaataatgcagctgtagctgtagatctcttgaggagcttcc 48600
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
584 accagggaccatttggggaagtgaatggaacttgatgacatgagctgctgc 535
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48601 ccaatggaataaagaagcaggttttgagatttcttgtagaggttacatt 48650
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
534 gttaggcagggagagagacagcaggaagccccaagacgatagcgcgaagatcc 485
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48651 ccaataagagaagaagctgcatactgcatctgcatctgcatcttattctgatat 48700
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
484 tgaaggcccgccgagctgctctgcagttt.....ggcgc 449
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48701 gacagttcctccactagatgctagtgaaagtttaaggtgtagcagggagagc 48750
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
448 ggaacgggtgttagatgtggccagctgacgctccacgctgacggtgtgtagt 399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48751 agaaataaggttgagcagcagctagcaattagagcaggttaaggccaccg 48800
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
398 ctgaagatgtgagcgaaacacacaggttctcaagaagagcgcttcttgaagta 349
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48801 gtgtatctgtgtgagagcagaagacttctgaaagtgcacactcttgact 48850
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
348 gcaagcccaagcgccgaacaagaagaaggtagtgtgcacaa.....tct 305
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48851 acttctcacaagccttgcctctagagtaacttcaactgtccagtgctctaa 48900
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
304 catagacctcaggggacattccaagagcagacacagcagaggtcagagacc 255
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48901 catctgactgcacatcagtgatcaagtgtacgtacataataatgtgtct 48950

```

```

254 gccaggtcgaagagtagtagtgtgtg.....ggcgtctcatagacctgg 210
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48951 tacactgagaagtaataaccactagatgaactctacgagagataataactct 49000
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
209 tgcctcagaatcacaacagcacaacagacaltgccaaltgacccaccac 160
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
49001 tctgttaacatttaggttcccttcacatcagtggaatagagctgtattaa 49050
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
159 aaaaattgacacatacacacacagacagcgaggaggaagaagtgtgtgcgc 110
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
49051 gtccaccagccttacatcagttccccaagtgaacaactcccccttggggn 49100
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
109 gaggctccgacagagaagccagatactcttcggtgtgtgttgagtggttc 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
49101 ggggggmgnggggggggggggggngngngnggtgtgtgtgtgtgtc 49150
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
59 tgaatgaticttctagtttctgtgtgtagatccagaagaatctctgaag 10
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
49151 gatnngaattgtnnctcngtctgaagngngngngngngngngatcatgt 49200
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
9 ttcttccat..... 1
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
49201 ctctgacctgaatgtgttttcttctcagacatactgcctccttgtat 49250

```

GAP of reverse of: us-09-684-725-1 check: 1088 from: 1 to: 729

FROM: /home/bobryen/big/US09684725.seq
Sequence 1, application us/09684725

General information:

Applicant: Lee Harland

Title of invention: novel polypeptide

File reference: pcs10361adam

to: version1 check: 7472 from: 64001 to: 96000

Symbol comparison table: /opt/gcg/gcgcore/data/rundata/nwsgapdna.comp
Compcheck: 8760

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: 0.000

Quality: 2425 Length: 32002

Ratio: 3.326 Gaps: 2

Percent Similarity: 34.938 Percent Identity: 34.938

Match display thresholds for the alignment(s):

1 = IDENTITY
5
1

us-09-684-725-1 x version1 September 12, 2001 10:38

```

729 .....ctagatcactctgagtgccatgaggtagtagagacacgtg 685
      | | | | | | | | | | | | | | | | | | | | | |
68401 tgactccataatcctagtaatgctccctccctgcaataaataatgaa 68450
      | | | | | | | | | | | | | | | | | | | | | |
684 gacagtcattggaggaggtagaatagaagaaggtgaccctgtagtga 635
      | | | | | | | | | | | | | | | | | | | | | |
68451 gtgtgctctgacaacacacctgtgtgcaagcactgtccctaactatc 68500
      | | | | | | | | | | | | | | | | | | | | | |
634 aattgtagatcacatggtctgtagaccgtacaggtgcccgaacctggg 585
      | | | | | | | | | | | | | | | | | | | | | |
68501 agatctgtgtgtgtgataccagacccctccagtgaaagtgcataag 68550
      | | | | | | | | | | | | | | | | | | | | | |
584 accagggaccattggggaagtgtggaactgtgtccatgtgactgtgt 535
      | | | | | | | | | | | | | | | | | | | | | |
68551 gtccagcccagaagtgatccagagacagcatagaanaatgattgtgg 68600
      | | | | | | | | | | | | | | | | | | | | | |
534 gtggcagaggagaagacaggaagcccagacgatgcccgaagatcc 485
      | | | | | | | | | | | | | | | | | | | | | |
68601 ggaacatttactcagcctcctctctgtgtgtagatgataaagatc 68650
      | | | | | | | | | | | | | | | | | | | | | |
484 tgaggcccgccggtgtgtgtgcaagttgtggtcggaacggtgtgag 435
      | | | | | | | | | | | | | | | | | | | | | |
68651 tacatgaggttaactcattccttactaataaccattataataacca 68700
      | | | | | | | | | | | | | | | | | | | | | |
434 atggccagctagcgtccacgctgacggtgtgtgtgtctgagtaggggc 385
      | | | | | | | | | | | | | | | | | | | | | |
68701 ctcatagatggaaaacatgaagcctaaagaatgtaaaaacagacaa 68750
      | | | | | | | | | | | | | | | | | | | | | |
384 gaaagcacacggctccaaagaagggcgtcttgaagtagacgccagggcc 335
      | | | | | | | | | | | | | | | | | | | | | |
68751 aggcagctactatataatagaaacttggccacaagctgcagcaacc 68800
      | | | | | | | | | | | | | | | | | | | | | |
334 cgaacaagaagaaggtagttgcgcacacatcicatgacctccaggggcat 285
      | | | | | | | | | | | | | | | | | | | | | |
68801 tggccagaagaacaaacttgcattactacatgaccagccagagaacca 68850
      | | | | | | | | | | | | | | | | | | | | | |
284 ccaaggagcagagacagaggtcagagaaccgacggctgaaaggtagta 235
      | | | | | | | | | | | | | | | | | | | | | |
68851 gcctgtgtlaagtcaggtctgtgaagaagctgtaactgtactttagtaa 68900

```

```

234 gtgtgtggcgtcttcataagcctgtgtgtgcagaataccaggcaca... 188
      | | | | | | | | | | | | | | | | | | | | | |
68901 aatctaggaagaagctaaacaataatcttctgttaacaatacagccccaatag 68950
      | | | | | | | | | | | | | | | | | | | | | |
187 ccaggacattgccaatgacccccaacaaanaaltggcacatacacca 138
      | | | | | | | | | | | | | | | | | | | | | |
68951 ccaggacttgacgaatga..cctagagttgattgagttccatgattttg 68998
      | | | | | | | | | | | | | | | | | | | | | |
137 gacacggggagaagaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 88
      | | | | | | | | | | | | | | | | | | | | | |
68999 gtccctatttccaaacttaggacccagcagagaagaatgaataagcttcc 69048
      | | | | | | | | | | | | | | | | | | | | | |
87 atactcctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 38
      | | | | | | | | | | | | | | | | | | | | | |
69049 caccatctcagagagctgctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 69098
      | | | | | | | | | | | | | | | | | | | | | |
37 gctgtagatccaggaagcattctgaagtgttccat..... 1
      | | | | | | | | | | | | | | | | | | | | | |
69099 ccagtagtctccaaacagccttcttcttcttcttcttcttcttcttct 69148

```

GAP of reverse of: us-09-684-725-1 check: 1088 from: 1 to: 729

FROM: of: /home/bobryen/Dig/US09684725.seq
sequence 1, application us/09684725

general information:

applicant: lee harland

file of invention: novel polypeptide

file reference: pcs10361adam

to: version1 check: 7472 from: 96001 to: 128000

Symbol comparison table: /opt/gcg/gcgcore/data/rundata/nwsgapdna.comp
CompCheck: 8760

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: 0.000

Quality: 2532 Length: 32009

Ratio: 3.473 Gaps: 6

Percent Similarity: 40.417 Percent Identity: 40.417

Match display thresholds for the alignment(s):

IDENTITY
1

us-09-684-725-1 x version1 September 12, 2001 10:53

```

729 .....ctagatactactctagtgcca 707
127201 atatgttgcatgcatcattagatcttgaacagattaaggctttaaa 127250
706 tgaagtagtaagaagacacttgatgacagtcacgtggagaggtagaatagg 657
127251 gcatcaaatcaaccagagaggtctctcgtggagaacagtcagaagcgg 127300
656 aagaggtgacctggaatgaatctgtagtc..cacatggcttgatg 609
127301 gggcagcagaagtggataaaaaaaacccggttaagaagctatttg 127350
608 accgtacaggtggccgaacctggagccaggga.....cccatggggaa 565
27351 atagaccaggtgggagaagaagtagcttgattagatgtagtcagaa 127400
564 gtaagtgaacttgatgcatgtgctgtgttggtggcaggagaaagca 515
127401 atgtttgagaagtgtcagaaggtgagaagtgtattcaggagatcaagaa 127450
514 cggagaagccccaagcagatgccgaagatccctgaaggcccgccgggtg 465
127451 agaaagtcttcaataga..gaggaagaatttaaaaaatcaatgc...tg 127495
464 ctctgcagtttggcgcgaaacgggtgtagatggtgccacgttagcgtc... 418
127496 ctgagaagttgaacaaagaagataaataattgataccttgaggtcatt 127545
417 .....cagcctgaagcgtgcatgctgagatgtaggcgaagcacacgg 374
127546 ggtgagcttgatgagagtggtcttcctctggaacaatgaaagaaagcctg 127595
373 tctcaaaagagggccgtcttgaagtagcagcccaaggccggaacaaga 324
127596 agtgaagtgatcccaagaaaggtgaatatgagatgtggagcaaaaaa 127645
323 gggtagtggccacatctcatagacctccagggtgcatccaaggagcag 274
127646 tatagatgagcaatttctgtagtctaaagaagcatatagagag 127695

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273 gaccagaagtcagaagaccgccaggctgaagaagtagtagtggggcg 224
127696 gattataacgattataacgtgaatgataataattacttaagtatataca 127745
223 tctcatagctgtgtgtcagaaatcaccaggcacacagagacattgccca 174
127746 tatattttaaacaacacacaaagaatgaagaatgtgcttatat 127795
173 atgacccaccacaaanaattggcacatcacccacagacagggagagaa 124
127796 tctctctctccattccatt....aactactcctcattgctcagggaagaa 127841
123 gaagtgtgtgcgcgaagggtccgacagaagagccagatactcctcgtgc 74
127842 aaagaccttcgtatgagatgggacaaaatgaccttgggagacacagc 127891
73 tgttaagtggttcttgaaatggaatctcttagttctgtctgttagatccag 24
127892 aggcacttgccttaagaagctctagatgagagcaggggttaaaa 127941
23 gaagattctgaagtcttcatt..... 1
127942 acagcagaacacactgagcaagcctctatgctcgttatagatctc 127991

```


GAP of reverse of: us-09-684-725-1 check: 1088 from: 1 to: 729
FROMIG of: /home/bobryen/b1g/US09684725.seq
sequence 1, application us/09684725

general information:
applicant: lee harland
title of invention: novel polypeptide
file reference: pcs10361adam

to: version1 check: 7472 from: 128001 to: 160000

Symbol comparison table: /opt/gcg/gcgcore/data/rundata/nwsgapdna.comp
Compcheck: 8760

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000
Quality:	2443	Length:	32006
Ratio:	3.351	Gaps:	6
Percent Similarity:	38.728	Percent Identity:	38.728

Match display thresholds for the alignment(s):

IDENTITY
1

us-09-684-725-1 x version1 September 12, 2001 10:45

```
729 .....ctagatactcactctgaagtcga 707
156251 aggttatttgaggatgacgtgagatcatcattataaagtatttgcacaa 156300
706 tgaagtagtagagacacttgacagtcacatgaggagaggtagaatag 657
156301 gtgcacaaagaaagtaactcaatattgttggctttaaatatagcata 156350
656 aaggaggtgacgtgagatgaaattgtagatccacatggct. tgaatga 608
156351 attgtaataagaaagcaaaagacaataatacaagaatgagctctgttg 156400
607 ccgtacacgggtgcccgaaccttggacacagggaacccattggggaaagtgg 558
556401 acaaaaatctctggaaacctgagtcagatcatattctggaagagtgaa 156450
557 aacttgatgcacatgacgtgtgttggcagggagaagagcacggagaa 508
156451 tatcttctaagatgaataataatagaagagatggaagg...gaaggtc 156496
507 gccccagaagatgcccgaagatccctgagggcccggcgggtgctctgca 458
156497 attccaagaagcaggtgtgacagcatggcggtcaaaggagcgccgagca 156546
457 gtttggcgcggaacgggtgtgagatgagccacgtagcgctccacgtgacg 408
156547 gtgtcttgaggtgacagagag..cgataagcagtgtagcttggagtcagag 156594
407 gttgtgattgctgagatggaagcgaaacacacgggtctcaagaagagccgt 358
156595 gtaaggatagtgagggcagatgaggggttggctctggaactccagcgcca 156644
357 ctltgaag.....tagcagcccacgggcccgaacaagaagaaggtagtgc 314
156645 cactaagattgtctgatatctgagggcccccacacaaaaaaataatt 156694
313 gccacatctctatagacctccaggggcatctcaagaagagcaccagagag 264
156695 ttgaaaaaaggggggccccaataaaggitttaagaggggggagcaaatgc 156744
```

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263 tcagagaccgccaagctgaagagtagtagttgttggcgcttccatagc 214
156745 tctgtctgcattttaagaagaatccctctgtgcatttgcacgcaggtgaa 156794
213 ctgtgtctgcagaatcaccaaggcacaccagacattgccaatg...acc 168
156795 tttaagaacaagaattcaggaagcagggagaaacaattagaagctgttgg 156844
167 cccacacaaaaattgacacatacacacacacggggaggaagaagt 118
156845 aatagttcagatgagaggtgagtgcacaaactgaactaaggcaatgtagca 156894
117 gctggccgaaggtccgacaggaaggccagatactcctcggtgttca 68
156895 gagacaaagagggaaataactataatgaataatttaagggtattcttaa 156944
67 ggtgttctctggaatgat..ctctagttctgtgtgtagatccaggaag 20
156945 aagatgtgagacatgattgattgacgttgaaggaaggttgccttgag 156994
19 catctgaagtttccat..... 1
156995 gttctgaccagtgcttaaatglaacgttggggcccttcaattaaagg 157044
```

GAP of reverse of: us-09-684-725-1 check: 1088 from: 1 to: 729

FROM: /home/bobryen/big/US09684725.seq
sequence 1, application us/09684725

general information:

applicant: lee harland

title of invention: novel polypeptide

file reference: pos10361adam

to: version1 check: 7472 from: 160001 to: 192000

Symbol comparison table: /opt/gcg/gcgcore/data/rundata/nwsgapdna.comp
CompCheck: 8760

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: 0.000

Quality: 2516 Length: 32002
Ratio: 3.451 Caps: 7

Percent Similarity: 41.816 Percent Identity: 41.816

Match display thresholds for the alignment(s):

IDENTITY
: 5
: 1

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```
729 .....ctagatactcaactctgagtcgcaatgaggtagtagagga 692
184301 ctccacaagcgtcgcatctccatccagagcatgacatctctt 184350
691 cactgagtcacagctggtgaggaagtagaataaggaaggtgacctg 642
184351 ctgggataaggaatctgtgtagtgaaactccctgactgcagtcac 184400
641 atgctg.....aaattgataccacatggcgttgatgacgtacag 600
184401 cataggtctctgcaggaagacacatcagcgtgtgtgctctctct 184450
599 gtgacgaacctg.....gaccaaggaccattggggaag 564
184451 gcggtccaaacctgcatctgttacaacatcctgcatgcaatttgtat 184500
563 tagtggaaactgtagtcagtgctgtgtggtggcagggaagagcac 514
184501 ttaaaataatcaggaagcatctcatcttattcgtagcaaatagttcag 184550
513 ggaagaagcccgacgaatgcttgaggatcccgccggtgctgc 464
184551 ggggtctccataacaaagcttcaagttcttaccagcatlta 184600
463 tctgagtttggcgggaacggtgtagatggtcagctagcgtccacg 414
184601 aaaaaaaatlaagcttaaccttctgtcagctgtatgacacaca 184650
413 ctgacggtggtgtagtcagtagtgagcgaagcacagcgtctcaagag 364
184651 gattcaaaatcaatctctcaa..gattccaacacagtcacagctatcc 184698
363 ggcgctcttgaaagtagcagccacggtgcccgaacagaagaaggtagtgc 314
184699 agaccatctgcataaagtcacataagtcacacccaagaacttactct 184748
313 gccacatctcagaacctccaggggcatctccaagagcaggaagcagagag 264
184749 ctgacataagaggtctcgtgtagccttaactaataatgcaatgacag 184798
```

```
263 tcaagagaccgc.....agctgaagaggtagtagtgtgtg 228
184799 atataaagacctcagactggaagagagaagtgaaagccctgttctg 184848
227 ggcgtctcatalagcctgtgtctgcagaataccacagccacacagacata 178
184849 tagttgtgtcagaatctgtgtgtgcagatgacagatggccgaataagt 184898
177 gccaatgacccccaacacaaaattgacacatacacacacagaacggtgga 128
184899 cacaagttccaacctgacctgtgtcatattcactacgtgatcttgt 184948
127 ggaagaagtgtgtgtgcgca.....gttcgcaagggaagccaga.... 87
184949 aaaaagaattccctcagcagattactagatctcagcgggtgccctgaaat 184998
86 ..tactctcgtgtgtgt.....caggtgttctggaatgatatc 48
184999 aagtacctcaggtgtattttatgtatccgtggaatttggagatcgt 185048
47 tctagttctgtgtgtagatccaggaagcattctgaagttttccat... 1
185049 tctaagttataagcctctcagaaccacataatgtgtgtcctccatgtg 185098
```

GAP of reverse of: us-09-684-725-1 check: 1088 from: 1 to: 729
FROMIG of: /home/bobryen/b1g/US09684725.seq
sequence 1, application us/09684725

general information:
applicant: lee harland
title of invention: novel polypeptide
file reference: pcs10361adam

to: version1 check: 7472 from: 192001 to: 218807

Symbol comparison table: /opt/gcg/gcgcore/data/rundata/nwsgapdna.comp
Compcheck: 8760

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000
Quality:	7290	Length:	26807
Ratio:	10.000	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

Match display thresholds for the alignment(s):

1 = IDENTITY
5 = 1

us-09-684-725-1 x version1 September 12, 2001 10:41

```
729 .....ctagatactact 717
204851 tgaataaagaaggatgctgctcagccaccagcctatgatactact 204900
716 ctgagtcgcaatgagtagtagagacacttgatgacatgctggggaagag 667
204901 ctgagtcgcaatgagtagtagagacacttgatgacatgctggggaagag 204950
666 gtagaataaggaaggatgacactgtagatgataaattgtagatccacatgg 617
204951 gtagaataaggaaggatgacactgtagatgataaattgtagatccacatgg 205000
616 gcttgatgaacggtacagtgtagcgaacctgtagaccaggaagaccattgggg 567
15001 gcttgatgaacggtacagtgtagcgaacctgtagaccaggaagaccattgggg 205050
566 aagtagtggaaacttgatgcaatgtagctgtgtgtggcaggaagaagag 517
205051 aagtagtggaaacttgatgcaatgtagctgtgtgtggcaggaagaagag 205100
516 caacgagaagcccccagacgaatgtagcgaagatcttgaaggcccgccggg 467
205101 caacgagaagcccccagacgaatgtagcgaagatcttgaaggcccgccggg 205150
466 tgcctcgaacttgtagcgaacgggtgtagatgtagccagtaagcgtcc 417
205151 tgcctcgaacttgtagcgaacgggtgtagatgtagccagtaagcgtcc 205200
416 acgctgacggtgtagcgaatgtagatgtagcgaagcacaacggtctcaaa 367
205201 acgctgacggtgtagcgaatgtagatgtagcgaagcacaacggtctcaaa 205250
366 gagggcggtcttgaatgtagcgaacgggcccgaacaagaaggtagt 317
205251 gagggcggtcttgaatgtagcgaacgggcccgaacaagaaggtagt 205300
316 tggccacacatctatagacctcaggggcatctcaagaagaagaccagg 267
205301 tggccacacatctatagacctcaggggcatctcaagaagaagaccagg 205350
```

```
266 aggtcagaacccgccaaggctgaagaagtagtagtggctggcgctctcat 217
205351 aggtcagaacccgccaaggctgaagaagtagtagtggctggcgctctcat 205400
216 agcctgtgtctgcaagaatcaccagggcacacacagaacatgtccaatgacc 167
205401 agcctgtgtctgcaagaatcaccagggcacacacagaacatgtccaatgacc 205450
166 ccaccacaaaattggcacaatacaccacagacaggggaagaagaatgg 117
205451 ccaccacaaaattggcacaatacaccacagacaggggaagaagaatgg 205500
116 ctgcccgaaggtccgcaagaaggacagatctcctcgtgctgttag 67
205501 ctgcccgaaggtccgcaagaaggacagatctcctcgtgctgttag 205550
66 gttttctggaatgatalcttctagtttctgtgtgttagatccagaagaat 17
205551 gttttctggaatgatalcttctagtttctgtgtgttagatccagaagaat 205600
16 tctgaagttttccat..... 1
205601 tctgaagttttccatccctgacatlaaataccaagcctgagcctccc 205650
```